

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	18	4 AAB49510	AAB49510 Adenoviru
2	85	100.0	18	5 ABB79304	Abb79304 E3/19K si
3	85	100.0	18	6 ABU87174	Abu87174 Adenoviru
4	85	100.0	18	8 ADN00512	Adn00512 E3/19K si
5	85	100.0	18	8 ADO55472	Ado55472 Murine E3
6	85	100.0	18	8 ADO43914	Ado43914 Amino aci
7	85	100.0	27	1 AAR63153	Aar63153 PLA tumou
8	85	100.0	27	2 AAY05400	Aay05400 T-cell Be
9	85	100.0	28	2 AAW81051	Aaw81051 Signal pe
10	85	100.0	48	6 ABU87179	Abu87179 Expressio
11	85	100.0	56	6 ABU87178	Abu87178 Carbhydr
12	85	100.0	90	3 AAY44364	Aay44364 KDEL rece
13	85	100.0	109	3 AAY44363	Aay44363 KDEL rece
14	85	100.0	109	3 AAY44365	Aay44365 KDEL rece
15	85	100.0	109	3 AAY44366	Aay44366 KDEL rece
16	82	96.5	26	6 ADA37032	Ada37032 Adenoviru
17	82	96.5	26	6 ADA37037	Ada37037 Minigene
18	81	95.3	17	2 AAR63147	Aar63147 Adenoviru
19	81	95.3	17	2 AAW81046	Aaw81046 Signal pe
20	81	95.3	17	3 AAY67363	Aay67363 Sorting s
21	81	95.3	27	2 AAW81049	Aaw81049 Signal pe
22	80	94.1	31	4 AAB35489	Aab35489 Internali
23	80	94.1	31	7 ADA88894	Ada88894 Internali
24	76	89.4	17	2 AAW81048	Aaw81048 Signal pe

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:04:17 ; Search time 76 Seconds  
 (without alignment)  
 104.063 Million cell updates/sec

Title: US-10-031-008-7

Perfect score: 85

Sequence: 1 MRYMTIGLLALAAVCSAA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\*

Maximum Match 100\*

Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2010s:\*

5: geneseqp2002s:\*

6: geneseqp2003s:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

## RESULT 1

AB49610 ID AA49610 standard; peptide; 18 AA.  
 XX  
 AC AC  
 XX DT 02-MAR-2001 (first entry)  
 XX Adenovirus B19 signal peptide sequence.  
 XX DB 42 45 52.9 3390 8 ADG93316  
 XX KW Antiangiogenic protein; viral particle; antitumour; pulmonary; cyostatic; antidiabetic; antineumatic; tumour; angiogenesis; metastasis; rheumatic disease; diabetic neovascularisation; haemopoiesis; wound healing; adenovirus; signal sequence.  
 XX KW  
 OS OS  
 XX PN WO20066379-11.  
 XX XX  
 XX PD 16-NOV-2000.  
 XX XX  
 XX PF 05-MAY-2000; 2000W0-US012392.  
 XX PR 07-MAY-1999; 99US-0133243P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Libutti SK, Feldman AJ,  
 XX XX DR WPI; 2001-016095/02.  
 XX PS Claim 22; Page 54; 78pp; English.

## SUMMARIES

This invention relates to a compound comprising a recombinant nucleic acid sequence encoding an antiangiogenic protein (e.g. endostatin) inserted within a viral nucleic acid sequence. The recombinant nucleic acid sequence is packaged in a virus particle, the expression of which results in the production of the antiangiogenic protein. The compound has antitumour; pulmonary; cytostatic; antidiabetic; and antirheumatic activity. The compound is useful for expressing an antiangiogenic protein in a cell to treat a tumour. The compounds can also be used for treating any disease or process mediated by angiogenesis such as leukaemia, metastasis, rheumatic diseases, diabetic neovascularisation, and antineoplastic agents.



CC binding, or inhibitors of receptor/ligand binding. The methods are also  
 CC useful for enhancing binding of anti-antigenic carbohydrate antibodies to  
 CC the antigenic carbohydrate in an individual, inhibiting binding of a  
 CC ligand to a receptor that is an antigenic carbohydrate, or identifying  
 CC peptide sequences that can induce an immune response. The minotype  
 CC peptides may be expressed from a vector as a fusion protein with  
 CC adenovirus E3 leader sequence and an HIV (human immunodeficiency virus) T  
 CC helper cell epitope. The present sequence is the adenovirus E3 leader  
 CC sequence. (Updated on 23-Oct-2003 to standardise OS field)

XX Sequence 18 AA;

Query Match Score 85; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILAAVCSAA 18

Db 1 MRYMILGILAAVCSAA 18

RESULT 4 ADN00612 standard; peptide: 18 AA.

XX ID ADN00612 standard; peptide: 18 AA.

XX AC ADN00612;

XX DT 17-JUN-2004 (first entry)

XX DB E3/19K signal sequence, SEQ ID 13.

XX PR 28-AUG-2002; 2002US-0406470P.

XX PA WO20040469-A2.

XX PN 20040469-A2.

XX PD 11-MAR-2004.

XX 27-AUG-2003; 2003WO-EP009497.

XX PR 28-AUG-2002; 2002US-0406470P.

XX PA (NOV) ) NOVARTIS AG.

XX PA (NOV) ) NOVARTIS PHARMA GMBH.

XX PI Campochiaro PA, Kaleko M;

XX WPI: 2004-239158-22.

XX Treating retinal detachment or retinal edema in an individual comprises increasing the amount of an endostatin in the ocular tissues of the individual to a retinal detachment- or retinal edema-inhibiting amount.

XX Example 1: SEQ ID NO 13; 48pp; English.

XX The present invention relates to a method for treating retinal detachment or retinal edema in an individual. The method comprises effecting an increase in the amount of an endostatin (ADN00600 or ADN00602) in ocular tissues of the individual to a retinal detachment- or retinal edema-inhibiting amount. The endostatin is used in manufacturing a medicament for the treatment of retinal detachment or retinal edema in an individual. In an example from the invention, the murine endostatin gene (ADN00612) was inserted upstream from the endostatin sequence by PCR using primers ADN00610 and ADN00613.

XX Sequence 18 AA;

Query Match Score 85; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILAAVCSAA 18

CC 1 MRYMILGILAAVCSAA 18  
 CC ||||| ||||| ||||| ||||| |||||  
 CC 1 MRYMILGILAAVCSAA 18  
 CC ||||| ||||| ||||| ||||| |||||

RESULT 5 AD055472 standard; peptide: 18 AA.

XX ID AD055472;

XX AC AD055472;

XX DT 15-JUL-2004 (first entry)

XX DE Murine E3/19K N-terminal peptide.

XX XX nitrogen monoxide; NO; signal cascade modulator;

XX KW human endostatin regulation; neuroprotective; nootropic;

XX KW cerebroprotective; vulnerable; cerebroprotective; protozoacide;

XX KW cyostatic; degenerative disease; infection; CNS; Alzheimer's disease;

XX KW cranial-cerebral trauma; cerebral tumour; glioblastoma;

XX KW astroblastoma; oligodendroglioma.

XX OS Mus sp.

XX PN DE10240735-A1.

XX XX PD 18-MAR-2004.

XX XX PF 29-AUG-2002; 2002DB-01040735.

XX XX PR 29-AUG-2002; 2002DB-01040735.

XX XX PA (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.

XX PI Deininger MH;

XX XX DR WPT; 2004-259561/25.

XX PR Regulating human endostatin expression, e.g. for treating CNS disorders or tumors, using nitrogen monoxide signal cascade modulators.

XX XX Example: Page 8; 18pp; German.

XX This invention describes the use of nitrogen monoxide (NO) signal cascade modulators in the production of medicaments for regulating human endostatin expression. The modulators described are NO synthase inhibitors, especially aminoguanidine, N(G)-nitro-L-arginine methyl ester (L-NAME), S-methyl-isothiourea, N(G)-monomethyl-L-arginine acetate (L-NNA), N(Gamma)-nitro-L-arginine, S-2-aminoethyl-isothiourea, S-ethyl-isothiourea, 2-amino-4-methyl-pyridine or L-N(6)-(1-minoethyl)-lysine.

XX The products of the invention have neuroprotective, nootropic, cerebroprotective, vulnerable, cerebroprotective, protozoacide and cyostatic activity. Where the modulators are NO synthase inhibitors or NO scavenging reagents, they are specifically used for treating degenerative diseases, and/or infections of the CNS, especially Alzheimer's disease, cranial-cerebral trauma or cerebral malaria. Where

CC the signal cascade modulators are NO donors or NO synthase stimulants,

CC they are specifically used for treating tumors, especially

CC glioblastomas, astroblastomas or oligodendrogliomas. The signal cascade

CC modulators are effective in regulating the levels of endostatin (a 20 kD

CC C-terminal fragment of collagen XVII), causing inhibition of angiogenesis

CC and tumor growth, without the need for external administration of

CC endostatin itself.

XX Sequence 18 AA;

Query Match Score 85; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILAAVCSAA 18

CC ||||| ||||| ||||| |||||  
 CC ||||| ||||| ||||| |||||

Query Match Score 85; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1 MRYMILGLALAAVCSAA 18	Query Match 100.0%; Score 85; DB 8; Length 18;
RESULT 6		Best Local Similarity 100.0%; Pred. No. 2.4e-06; Mismatches 0; Indels 0; Gaps 0;
ADO43914	ADO43914 standard; peptide; 18 AA.	
ID		
XX		
AC	ACD43914;	
XX		
DT	15-JUL-2004 (first entry)	
XX		
DB	Amino acid sequence of the E3/19K signal peptide.	
XX		
KW	retina; endostatin; vascular endothelial growth factor receptor;	
KW	pigment epithelium-derived factor; angiostatin; plasminogen fragment;	
KW	rod-derived cone viability factor; antiangiogenic antithrombin;	
KW	cartilage-derived inhibitor; CD59 complement Fragment;	
KW	fibronectin fragment; Gro-beta; heparinase; chorionic gonadotropin;	
KW	interferon; interferon inducible protein; IP-10; interleukin-12;	
KW	kringle 5; metalloproteinase inhibitor; Placental ribonuclease inhibitor;	
KW	plasminogen activator inhibitor; platelet factor-4; PRP; prolactin;	
KW	proliferin-related protein; PRP; thrombospondin-1; TSP-1;	
KW	transforming growth factor-beta; TGF-b; vasolectatin; vasostatin;	
KW	calreictulin; retinal disorder; retinal detachment; diabetic retinopathy;	
KW	retinal neovascularization; choroidal neovascularization; retinal edema.	
XX		
OS	unidentified adenovirus.	
XX		
PN	OS Homo sapiens.	
XX		
PD	Synthetic.	
XX		
PN	WO2004028635-A1.	
XX		
PD	08-APR-2004.	
XX		
PP	26-SEP-2003; 2003WO-EP010725.	
XX		
PR	27-SEP-2002; 2002US-0414048P.	
XX		
PA	NOVARTIS AG.	
PA	(NOVS ) NOVARTIS PHARMA GMBH.	
PA	Campochiaro PA, Kaleko M;	
PI		
XX		
DR	WPI; 2004-305131/28.	
XX		
PR	Example 1: Page 11; 47PP; English.	
PR	Delivering a protein to the retina of a subject for treating retinal	
PR	disorders, e.g., retinal detachment, retinal edema or diabetic	
PR	retinopathy by periodically injecting a viral vector comprising a protein	
PR	-encoding nucleic acid.	
XX		
PS	Example 1: Page 11; 47PP; English.	
XX		
CC	The specification describes a method for delivering a protein to the retina of a subject. The method comprises periodically injecting a viral vector comprising a nucleic acid encoding endothelial growth factor receptor, pigment epithelium-derived factor, angiostatin (plasminogen fragment), rod-derived cone viability factor, antiangiogenic antithrombin III, cartilage-derived inhibitor (GDI), CD59 complement fragment, fibronectin fragment, Gro-beta, a heparinase, human chorionic gonadotropin (hCG), an interferon, interferon inducible protein (IP-10), interleukin-12, kringle 5 (plasminogen fragment), metalloproteinase inhibitors (TBV18s), placental ribonuclease inhibitor, plasminogen activator inhibitor, platelet factor-4 (PF4), prolactin (PRP), thrombospondin-1 (TSP-1), transforming growth factor-beta (TGF-b), vasolectatin or vasostatin (calreticulin fragment). The method is useful in delivering a protein to the retina of a subject for treatment of retinal disorders, e.g., retinal detachment, diabetic retinopathy, retinal neovascularization, choroidal neovascularization or retinal edema. The present signal peptide was attached to murine endostatin, and used to construct viral vectors for use in the method of the invention.	
CC	Sequence 18 AA;	
SQ	Sequence 27 AA;	
Db	1 MRYMILGLALAAVCSAA 18	Query Match 100.0%; Score 85; DB 2; Length 27;
XX		Best Local Similarity 100.0%; Pred. No. 3.7e-06; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MRYMILGLALAAVCSAA 18	
Db	1 MRYMILGLALAAVCSAA 18	





subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromyoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide, the oligomerisation domain of human phospholamban (PLB) pentamerisation domain; a camel IgG linker domain and the carboxy-terminal sequence GDCG. The subsequence GDCG is an alteration of rat carboxy oligomeric matrix protein which provides increased stability via disulphide bonds. (Updated on 12-SEP-2003 to standardise CS field)

Disclosure: Fig 6; 87pp. English.

The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astrocytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable oligomeric matrix peptid: the oligomerisation domain of human cartilage oligomeric matrix protein (COMP) pentamerisation domain, a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GBCC is an alteration of rat COMP which provides increased stability via disulphide bonds.

(Updated on 12-SEP-2003 to standardise OS field)

Sequence 109 AA;		Query Match		Score 85; DB 3; Length 109;			
		Best Local Similarity	100.0%	Pred. No.	1.7e-05;		
		Matches	18;	Mismatches	0;	Indels	0;
		Conservative	0;				Gaps
1	MRYMTIGLIALAAVSSAA	18					0
1	MRYMTIGLIALAAVSSAA	18					

RESULT 14  
 AAY44965 AAY44965 standard; protein; 109 AA.  
 {  
 AAY44965;  
 { 12-SEP-2003 (revised)  
 23-MAY-2000 (first entry)  
 KDEL receptor inhibitor protein-8.

Key	Location/Qualifiers
Peptide	1 .. 20 /label = "Signal Peptide" /note = "Derived from adenovirus E3"
Domain	30 .. 75 /note = "Human TSP 3 trimerisation domain"
Domain	.99 .. .99 /note = "[Camel] TGF linker domain"

WO200006729-A1.  
10-FEB-2000.  
28-JUL-1999; 99WO-US017147.  
29-JUL-1998; 98US-00124671.  
(SLOK ) SLOAN KETTERING INST CANCER RES.  
Portman, TR Matthew M. Hoe MH.

WPI: 2000-195236/17.  
N-PSDE; AAZ50499.  
Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell.

The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and

23-MAY-2003	(LAST ENTRY)
QX	KDEL receptor inhibitor protein-9.
DE	KDEL receptor inhibitor; heat shock protein; immune response;
QX	oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;
KW	melanoma; carcinoma; glioblastoma; astromyoma; oncogene;
KW	infectious disease; allergy; autoimmune disease.
QX	unidentified adenovirus; B3.
DS	<i>Homo sapiens</i> .
DS	<i>Camelus</i> sp.
DS	Chimeric.
QX	

XX  
PP 28-JUL-1999; 99WO-US017147.  
XX  
PR 29-JUL-1998; 98US-00124671.  
XX  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX  
PI Rothman JB, Mayhew M, Hoe MH;  
XX  
DR WPI; 2000-185296/17.  
XX  
N-PSDB; AAZ20500.  
XX  
Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell.  
XX  
Disclosure: Fig 9; 87pp; English.  
XX  
The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, melanoma, carcinoma, glioblastoma and astrocytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human thrombospondin 4 (TSP4) trimerisation domain, a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequent G'DCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 109 AA:

Query Match 100.0%; Score 85; DB 3; Length 109;  
Best Local Similarity 100.0%; Pedi. No. 1.7e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MRYMILGILALAAVCSAA 18  
Db 1 MRYMILGILALAAVCSAA 18

Search completed: January 11, 2006, 00:08:16  
Job time : 77 secs

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Qy 2 RYML--GILLAAYCS 16  
Db 141 RYLLITYGFLCLASVCS 157

RESULT 5  
T43290  
hemicentin precursor - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43290; R20993; T24734  
R;Vogel, B.E.; Hedgecock, E.M.  
C;Accession: D83173  
C;Description: Hemimentin is required for hemidesmosome mediated cell adhesion and germ-  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br-  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho-  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: D83173  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-131 <STO>  
A;Cross-references: UNIPARC:Q9HKK7; UNIPARC:UPI00000C5B13; GB:AE004797; GB:AE004091; NID  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3788

Query Match 54.1% Score 46; DB 2; Length 131;  
Best Local Similarity 56.2%; Pred. No. 7.3;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RYMLGHLAAVCSA 17  
Db 70 RYLVGLHLAAVATAS 85

RESULT 4  
T20992  
hypothetical protein F15G9.4a - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T20992; T24733  
R;Sulston, J.  
Submitted to the EMBL Data Library, December 1994  
A;Reference number: Z19355  
A;Status: Preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-5198 <WIL>  
A;Cross-references: UNIPARC:UPI0000110172; EMBL:247068; PIDN:CAA87335.1; GSPDB:GN00028;  
A;Experimental source: clone F15G9  
C;Genetics:  
A;Gene: him-4; F15G9.4b  
A;Map position: X  
A;Introms: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;  
A;Accession: T24734  
A;Status: Preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-5198 <WIL2>  
A;Cross-references: UNIPARC:UPI0000110172; EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028;  
A;Experimental source: clone T09B9

Query Match 54.1% Score 46; DB 2; Length 5198;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 YMILGLHLAAVCSA 17  
Db 9 YGVGLHLATTCS 23

RESULT 6  
ERADAS  
early E3 18.5K glycoprotein - human adenovirus 5  
C;Species: Mastadenovirus hs (human adenovirus 5)  
A;Note: host: Homo sapiens (man)  
C;Date: 17-Mar-1997 #sequence\_revision 17-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: A03822; A22515  
R;Cladaras, C.; Wold, W.S.M.  
Virology 140, 28-43, 1985  
A;Title: DNA sequence of the early E3 transcription unit of adenovirus 5.  
A;Reference number: A94333; MUID:85092388; PMID:2981456  
A;Map position: X  
A;Introms: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;  
A;Accession: T24733  
A;Status: Preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-5175 <WIL>  
A;Cross-references: UNIPARC:UPI00001101B6; EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028;  
A;Experimental source: clone T09B9  
C;Genetics:  
A;Gene: CE3P:F15G9.4a  
A;Map position: X  
A;Introms: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;  
A;Accession: T24733  
A;Status: Preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-5175 <WIL>  
A;Cross-references: UNIPARC:UPI00001129AE7; GB:X03002; NID:958503; PIDN:(  
R;Wold, W.S.M.; Cladaras, C.; Deutscher, S.L.; Kapoor, Q.S.  
J. Biol. Chem. 260, 2424-2431, 1985  
A;Title: The 19-kDa glycoprotein coded by region B3 of adenovirus.  
A;Reference number: A22515; MUID:85130985; PMID:3882694  
A;Accession: A22515  
A;Molecule type: DNA  
A;Residues: 1-160 <WIL>

Qy 3 YMILGLHLAAVCSA 17  
Db 9 YGVGLHLATTCS 23

A;Cross-references: UNIPARC:UPI000129AB7; GB: M12406; PIDN: g209911; PID: A;Status: preliminary  
 C;Superfamily: adenovirus early B3 18.5K glycoprotein, transmembrane protein  
 C;Keywords: early protein; Glycoprotein  
 F;30,79/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 P;30,79/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.9%; Score 45; DB 1; Length 160;  
 Best Local Similarity 69.2%; Pred. No. 12;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 A;Map position: 5  
 A;Introns: 44/2; 8/3  
 A;Note: T7H20.110

Qy 1 MRYMILGILALAA 13  
 :||:|||:|||:  
 Db 2 IRYVILGILTLAS 14

RESULT 7  
 GRWVD3 genome polyprotein - dengue virus type 3  
 N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS5  
 a; nonstructural protein NS1b; nonstructural protein NS5  
 C;Species: dengue virus type 3  
 C;Accession: A34774  
 C;Cross-references: UNIPROT:P27915; UNIPARC:UPI000131DFE; GB:M93130; PIDN: A;Reference number: A34774; PMID:90266483; PMID:2345967  
 A;Molecule type: genomic RNA  
 A;Residues: 1-3390 <OSA>  
 C;Superfamily: hepatitis C virus genome polyprotein  
 C;Keywords: Atp; capsid protein; envelope protein; glycoprotein; nonstructural protein;  
 P;1-114/Domain: capsid protein #status predicted <TM1>  
 P;16-67/Domain: transmembrane #status predicted <TM1>  
 P;115-280/Product: membrane protein precursor #status predicted <MRP>  
 P;115-205/Domain: non-terminal signal sequence #status predicted <SIG>  
 P;206-280/Product: membrane protein #status predicted <MEN>  
 P;266-280/Domain: transmembrane #status predicted <TM3>  
 P;281-73/Product: envelope protein #status predicted <ENV>  
 P;724-746/Domain: transmembrane #status predicted <TM4>  
 P;753-771/Domain: transmembrane #status predicted <TM5>  
 P;774-1184/Domain: non-structural protein NS1 #status predicted <NS1>  
 P;1156-1175/Domain: transmembrane #status predicted <TM6>  
 P;1185-1343/Product: nonstructural protein NS2a #status predicted <N2A>  
 P;1344-1433/Product: nonstructural protein NS2b #status predicted <N2B>  
 P;1474-2092/Product: nonstructural protein NS3 #status predicted <NS3>  
 P;1667-1674/Region: nucleotide-binding motif A (P-loop) predicted A  
 P;1754-1759/Region: nucleotide-binding motif B  
 P;1758-1761/Region: DEAH motif  
 P;2093-3378/Product: nonstructural protein NS4a #status predicted <N4A>  
 P;2379-2490/Product: nonstructural protein NS4b #status predicted <N4B>  
 P;2491-3390/Product: nonstructural protein NS5 #status predicted <NS5>  
 P;183,347,433,750,903,980,1132,1188,1661,2300,2304,2386,2456,2702,2712/Binding site: car

Query Match 52.9%; Score 45; DB 1; Length 3390;  
 Best Local Similarity 41.2%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 A;Map position: 5  
 A;Introns: 44/2; 8/3  
 A;Note: T7H20.110 #text\_change 09-Jul-2004

Qy 1 MRYMILGILALAA 17  
 :||:|||:|||:  
 Db 2226 LAYVVGILTLAAVAA 2242

RESULT 8  
 T48227 hypothetical protein T7H20.110 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C;Accession: T48227  
 R;Bayan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stielkema, W.; Bancroft, I.; Mek  
 Submitted to the Protein Sequence Database, March 2000  
 A;Reference number: Z24488  
 A;Accession: T48227

A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-152 <BBV>  
 A;Cross-references: UNIPROT:Q91ZM5; UNIPARC:UPI0000A7FB; EMBL:AU162508  
 A;Experimental source: cultivar Columbia; BAC clone T7H20  
 C;Genetics:  
 A;Map position: 5  
 A;Introns: 44/2; 8/3  
 A;Note: T7H20.110

Query Match 51.8%; Score 44; DB 2; Length 152;  
 Best Local Similarity 64.3%; Pred. No. 16;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TIGLILALAAVCSAA 18  
 :|||:|||:  
 Db 89 VIALLALAAACSSA 102

RESULT 9  
 E72522 hypothetical protein APE2154 - Aeropyrum pernix (strain K1)  
 C;Species: Aeropyrum pernix  
 C;Accession: E72522  
 C;Cross-references: UNIPROT:Q9V9Y5; UNIPARC:UPI00005E229; DDBJ:AP000063; NID:95105654;  
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix K1  
 A;Reference number: A72450; PMID:99310339; PMID:10382966  
 A;Accession: E72522  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-255 <KAV>  
 A;Cross-references: UNIPROT:Q9V9Y5; UNIPARC:UPI00005E229; DDBJ:AP000063; NID:95105654;  
 A;Experimental source: strain K1  
 C;Genetics:  
 A;Gene: APE2154  
 C;Superfamily: conserved hypothetical protein HI0188

Query Match 51.8%; Score 44; DB 2; Length 255;  
 Best Local Similarity 66.7%; Pred. No. 24;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RYMLGLLAAVCSA 16  
 :|||:|||:  
 Db 198 RMVILGLLALGAVS 212

RESULT 10  
 D87575 hypothetical protein CC2633 [imported] - Caulobacter crescentus  
 C;Species: Caulobacter crescentus  
 C;Accession: D87575  
 C;Cross-references: D87575  
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.T.; Heidelberg, J.  
 B.; Lubin, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo  
 n, J.; Embleva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.  
 A;Title: Complete Genome Sequence of Caulobacter crescentus  
 A;Reference number: A87249; PMID:11259567  
 A;Accession: D87575  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-334 <STO>  
 A;Cross-references: UNIPROT:Q9A536; UNIPARC:UPI0000C77B7; GB:AE005673; NID:913424210;  
 C;Genetics:  
 A;Gene: CC2633

Query Match 51.8%; Score 44; DB 2; Length 334;  
 Best Local Similarity 50.0%; Pred. No. 30;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

3 YMIGLGLAAAVCSAA 18  
 : ||| :| :| ||| |  
 9 FVAGLMAMLMACSPA 24

RESULT 11

AB0276 probable membrane protein YPO2266 [imported] - *Yersinia pestis* (strain C932)  
 C;Species: *Yersinia pestis*  
 C;Accession: AB0276  
 C;Cross-references: UNIPROT:Q8ZEB5  
 C;Gene: YP02266  
 C;Superfamily: probable antibiotic resistance protein YybF  
 C;Genetics:

Query Match Score 44; DB 2; Length 742;  
 Best Local Similarity 51.8%; Pred. No. 54;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 Qy 2 RYMIGLGLAAVCSAA 18  
 Db 9 RRSLLGILAACTICAAA 25

RESULT 14

GB3476 hypothetical protein PA1343 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
 C;Species: *Pseudomonas aeruginosa*  
 C;Accession: GB3476  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Britton, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
 A;Reference number: MUID:21470413; PMID:11586360  
 A;Accession: AB0276  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-372 <KUR>  
 A;Cross-references: UNIPROT:Q8ZEB5; UNIPARC:UPI00000CD8C9; GB:AL590842; PMID:CAC91070.1;  
 C;Gene: YP02266  
 C;Superfamily: probable antibiotic resistance protein YybF  
 C;Genetics:

Query Match Score 44; DB 2; Length 372;  
 Best Local Similarity 51.8%; Pred. No. 32;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 4 MIIGLGLAAVC 15  
 Db 206 LVIGLGLAAAC 217

RESULT 12

A49340 alcohol dehydrogenase (EC 1.1.1.1) precursor - *Acetobacter pasteurianus* (strain NCI1380)  
 C;Species: *Acetobacter pasteurianus*  
 C;Accession: A49340  
 C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 05-Oct-2004  
 R;Takemura, H.; Kondo, K.; Horinouchi, S.; Beppu, T.  
 J;Bacteriol. 175, 6857-6866, 1993  
 A;Title: Induction by ethanol of alcohol dehydrogenase activity in *Acetobacter pasteurianus*  
 A;Reference number: MUID:94042848; PMID:8226628  
 A;Accession: A49340  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-742 <TAK>  
 A;Cross-references: UNIPROT:Q53362; UNIPARC:UPI00000BDE0D; GB:D13893; MUID:9517067; PIDN:  
 C;Keywords: Glucose/Alcohol /Shikimate dehydrogenase  
 C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match Score 44; DB 2; Length 742;  
 Best Local Similarity 51.8%; Pred. No. 54;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 Qy 2 RYMIGLGLAAVCSAA 18  
 Db 9 RRSLLGILAACTICAAA 25

RESULT 15

T25247 hypothetical protein T24F1.5 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Accession: T25247  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 R;Chui, C.  
 submitted to the EMBL Data Library, June 1995  
 A;Reference number: Z20004  
 A;Accession: T25247  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-64 <WIL>  
 A;Cross-references: UNIPROT:Q22746; UNIPARC:UPI0000076473; EMBL:249912; PIDN:CAA90139.1,  
 C;Genetics:

RESUL 13  
 JS0326 alcohol dehydrogenase (EC 1.1.1.1) 72K chain precursor - *Acetobacter aceti*  
 C;Species: *Acetobacter aceti*  
 C;Accession: JS0326  
 C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 05-Oct-2004  
 R;Inoue, T.; Sunagawa, M.; Mori, A.; Imai, C.; Fukuda, M.; Takagi, M.; Yano, K.  
 J;Bacteriol. 171, 3115-3122, 1989  
 A;Title: Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase subunit  
 A;Accession: JS0326  
 A;Reference number: MUID:89255070; PMID:272742  
 A;Cross-references: UNIPROT:Q53362; UNIPARC:UPI00000BDE0D; GB:D13893; MUID:9517067; PIDN:  
 C;Keywords: Glucose/Alcohol /Shikimate dehydrogenase  
 C;Keywords: alcohol metabolism; NAD; oxidoreductase

	Matches	9;	Conservative	3;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	MRVMILGILAVCSA	17	:		:				
Db	1	MRPVLALVLVLPATQA	17							

Search completed: January 11, 2006, 00:10:05  
Job time : 17 secs

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Gapopen:	10.0						
Gapext:	0.5						
Searched:	2166443 seqs, 705528306 residues						
Total number of hits satisfying chosen parameters:	2166443						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0%						
	Maximum Match 100%						
	Listing first 45 summaries						
Database :	UniProt 05_80:*						
	1: uniprot_sprot;*						
	2: uniprot_trembl;*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query	Match	Length	DB	ID	Description
1	85	100.0	159	1	B3GL_ADE02	P69978	human adeno
2	85	100.0	159	1	B3GL_ADE06	P69979	human adeno
3	85	100.0	159	2	091074_ADE02	091024	human adeno
4	85	100.0	159	2	077985_ADE02	077995	human adeno
5	64	75.3	160	2	012399_ADE01	012399	human adeno
6	54	63.5	81	2	075WH5_MACGS	075WH5	macrophile
7	51	60.0	179	2	Q9SP73_HAEIR	Q9SP73	haemacobia
8	51	60.0	208	2	Q7Q1D4_ANOGR	Q7Q1D4	anophales g
9	51	60.0	294	2	076XK1_SNVPX	076XK1	synecchococcus
10	49	57.6	110	2	Q5FP07_GLUCK	Q5FP07	gluconobact
11	49	57.6	294	2	Q4USU3_XANCP	Q4USU3	xanthomonas
12	49	57.6	294	2	Q8PB18_XANCP	Q8PB18	xanthomonas
13	48	56.5	181	2	Q9V523_DROME	Q9V523	drosophila
14	48	56.5	188	2	Q95T42_DROME	Q95T42	drosophila
15	48	56.5	250	2	Q5U195_DROME	Q5U195	drosophila
16	48	56.5	490	2	Q9V1V5_DROME	Q9V1V5	drosophila
17	48	56.5	557	2	Q5NR85_ZYMO	Q5NR85	zymomonas m
18	47.5	55.9	135	1	1IL5_CAVPO	008387	cavia porce
19	47	55.3	466	2	Q18472_CAEEL	Q18472	canonohabdi
20	47	55.3	471	2	Q5AXY5_EMENTI	Q5AXY5	aspergillus
21	47	55.3	646	2	Q6Y752_ORYSA	Q6Y752	oryza sativ
22	47	55.3	647	2	Q84ZH7_ORYSA	Q84ZH7	oryza sativ
23	46	54.1	131	1	Q9HXXK7_PSEAB	Q9HXXK7	pseudomonas
24	46	54.1	140	2	Q82PKU_STRAW	Q82PKU	streptomyce
25	46	54.1	310	2	Q8MVK4_9ASCI	Q8MVK4	boltenia vi
26	46	54.1	455	2	Q8G7J6_BIFLO	Q8G7J6	bifidobacte
27	46	54.1	523	2	Q9V1V4_DROME	Q9V1V4	drosophila
28	46	54.1	595	2	Q4V5Q7_DROME	Q4V5Q7	drosophila
29	46	54.1	1895	1	Q7R599_GIALLA	Q7R599	giardia lam
30	46	54.1	2258	1	P01_BAMMN	P0245	b genome
31	46	54.1	2258	2	Q55455_9POTY	Q55455	barley mild

GenCore version 5.1.6  
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OM protein - protein search, using SW mode!

Run on: January 11, 2006, 00:04:42 ; Search time 71 Seconds  
(without alignments)  
178.866 Million cell updates/sec

Title: US-10-031-008-7  
Perfect score: 85  
Sequence: 1 MRYMTGLLALAAYCSAA 18

Scoring table: BLOSUM62  
Gapopen 10.0 , Gapext 0.5

ALIGNMENTS

Total number of hits satisfying chosen parameters:

RESULT 1  
EGL\_ADE02

ID EGL\_ADE02 STANDARD;

AC P69978; P03251;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DB E.3 18.5 kDa glycoprotein precursor (GP19K) (E3-19K) (E3gp 19-

kDa) (B19).

DE Human adenovirus 2 (HAdV-2)

OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI\_TaxID=10515;

RN [1];

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE-810130985; PubMed=6253880;

RA Herisse J., Courtois G., Galibert F.

RT "Nucleotide sequence of the E3 of adenovirus 2 genome.";

RL Nucleic Acids Res. 8:2173-2192 (1980).

RN PROTEIN SEQUENCE OF N-TERMINUS, AND N-GLYCOSYLATION.

RX MEDLINE-85130985; PubMed=3182694;

RA Wold W.S.M., Cladaras C., Deutscher S.L., Kapoor Q.S.;

RT "The 19-kDa glycoprotein coded by region E3 of adenovirus.

RT Purification, characterization, and structural analysis.";

RL RN [2];

RP DISULFIDE BONDS, AND MUTAGENESIS OF CYS-28; CYS-39; CYS-45; CYT-100;

RA CVS-118; CVS-126 AND CVS-139.

RT PubMed=1057124;

RX RA Sester M., Burger H.-G.;

RT "Conserved cysteine residues within the E3/19K protein of adenovirus

type 2 are essential for binding to major histocompatibility complex

RT type 2 are essential for binding to major histocompatibility complex

RT RT antigens.";

RT R. Virol. 68:5423-5432 (1994).

CC -1- FUNCTION: Binds and retains class I heavy chains in the endoplasmic reticulum during the early period of virus infection. Also delays thereby impairing their transport to the cell surface. Also delays the expression of class I alleles that it cannot affect by direct retention.

CC Binds transporters associated with antigen processing (TAP) and acts as a tapasin inhibitor, preventing class I/TAP

CC association. In consequence, infected cells are masked for immune

CC recognition by cytotoxic T lymphocytes (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic

CC reticulum.

CC -1- DEVELOPMENTAL STAGE: Expressed at early period of virus infection.

CC -1- DOMAIN: The luminal domain binds directly to the peptide-binding

CC domain of class I molecules.

CC -1- PTM: Both disulfide bonds are absolutely critical for the

CC interaction with MHC antigens.

CC -1- PTM: N-Glycosylated; high-mannose.

CC -1- SIMILARITY: Belongs to the adenoviruses E19 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC



RESULT 4	Q779F5_ADB02	PRBLIMINARY;	PRT;	159 AA.
ID	Q779F5_ADB02			
AC	Q779F5;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	10-MAY-2005 (TREMBLrel. 30, Last annotation update)			
DB	19K Glycoprotein.			
OS	Human adenovirus 2 (HAdV-2).			
OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.			
OX	NCBI_TaxID=10515;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE	Bar swab, Respiratory epithelium, and Stool sample;		
RC	Borcherding P., Pring-Akerblom P.;			
RA	TISSUE-Liver, Bar swab, Respiratory epithelium, and Stool sample;			
RA	Borcherding P., Pring-Akerblom P.;			
RL	Submitted (SEB-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ231913; CAC67703_1; -; Genomic_DNA.			
DR	EMBL; AJ231914; CAC67712_1; -; Genomic_DNA.			
DR	EMBL; AJ231916; CAC67728_1; -; Genomic_DNA.			
DR	EMBL; AJ231917; CAC67736_1; -; Genomic_DNA.			
DR	EMBL; AJ231912; CAC67695_1; -; Genomic_DNA.			
DR	GO; GO:0005515; F:mannose binding; IEA.			
DR	GO; GO:0005690; F:protein binding; IEA.			
DR	InterPro; IPR006965; Adeno_GP19K.			
DR	PFAM; PF0488; Adeno_GP19K.			
SQ	SEQUENCE	18438 AA; 18438 MW; BD2519547E18AEBO CRC64;		
Qy	1 MRYMILGLLLAAVCsAA 18			
Db	2 IKVILSLLTLAAVCsAA 19			
RESULT 6	Q77WHS_MACGS PRELIMINARY;	PRT;	81 AA.	
ID	Q77WHS_MACGS PRELIMINARY;			
AC	Q77WHS;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Peptide toxin 2.			
DE	Macrothele gigas (Spider).			
OS	Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;			
OC	Mygalomorphae; Hexathelidae; Macrothele.			
NCBI_TaxID=223896;				
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Venom Gland;			
RA	Satoh H., Villegas E., Corzo G.,			
RA	Submitted (SEB-2003) to the EMBL/GenBank/DBJ databases.			
RL	Submittet (SEB-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB121196; BAD13403_1; -; mRNA.			
DR	GO; GO:0009405; P:Pathogenetic_s; IEA.			
DR	InterPro; IPR011696; Toxin_12.			
DR	PFAM; PF07740; Toxin_12; 1.			
SQ	SEQUENCE	81 AA; 9042 MW; 534E7162AC41ECFB CRC64;		
Qy	1 MRY - MILGLLLAAVCsAA 18			
Db	1 MRYMILGLLLAAVCsAA 18			
RESULT 5	Q12399_ADB01	PRT;	160 AA.	
ID	Q12399_ADB01 PRELIMINARY;			
AC	Q12399;			
DT	01-JUL-1997 (TREMBLrel. 04, Created)			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-MAY-2005 (TREMBLrel. 30, Last annotation update)			
DB	Gp19K protein (Glycosylated membrane protein 18.6 kDa).			
GN	Name-Ad1/83-8P19K;			
OS	Human adenovirus 1 (HAdV-1)			
OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.			
NCBI_TaxID=10533;				
OX	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Hannover/Adrian German reference center for adenoviruses;			
RA	Reichmann H., Schaarschmidt E., Geisler B., Haussmann J., Orthmann D.,			
RA	Bauer U., Plunker G., Seidel W.;			
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.			
RN	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Hannover/Adrian German reference center for adenoviruses;			
RA	Reichmann H., Schaarschmidt E.,			
RA	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	PubMed=15302955; DOI=10.1099/vir.0.80118-0;			
RA	Lauer K.P., Llorente I., Blair E., Seto J., Krasnov V., Tibbott C.,			
RA	Purkayastha A., Ditty S.E., Hadfield T.L., Buck C., Tibbott C.,			
RA	Seto D.;			
RT	"Natural" variation among human adenoviruses: genome sequence and			
RT	annotation of human adenovirus serotype 1."			
RT	annovation of human adenovirus serotype 1."			
RL	J. Gen. Virol. 85:2615-2625(2004);			
DR	EMBL; Y11260; CAA72130_1; -; Genomic_DNA.			
DR	EMBL; AF534906; AAC101059_1; -; Genomic_DNA.			
DR	EMBL; AF534906; AAC101059_1; -; Genomic_DNA.			
DR	SEQUENCE	179 AA; 19910 MW; 86710AE8A1ADCBFA CRC64;		

Query Match	Score 51; DB 2; Length 179;	DR	GO:0005524; F:ATP binding; IEA.
Best Local Similarity	53.1%;	DR	GO:0042626; F:ATPase activity, coupled to transmembrane m. . . ; IEA.
Matches	Pred. No. 17;	DR	GO:0006610; F:ATPase activity, IEA.
Matches	6; Mismatches 1; Indels 0;	DR	GO:0042626; F:ATPase activity, IEA.
Qy	3 YMIGLLAAYCSA 17	DR	InterPro:IPR001626; ABC_3.
	:::  :  :  :	DR	Pfam:PF00950; ABC_3; 1
Db	8 FVVGILALSACQAA 22	KW	Complete proteome; Transmembrane; Transport
		SQ	SEQUENCE 294 AA; 31407 MW; BPP5B7C298629D4 CRC64;
RESULT 8		Query Match	Score 51; DB 2; Length 294;
Q7QID4_ ANOGA PRELIMINARY;	PRT; 208 AA.	Best Local Similarity	60.0%;
ID Q7QID4_		Pred. No. 25;	
AC		Mismatches	3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)		Indels	0;
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)		Gaps	0;
DE ENSANGP0000001405 (Fragment) .			
GN ORFName=B-ENSANGC00000010916;			
OS Anopheles gambiae str. PEST.			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;			
OC Anophelinae; Anopheles.			
NCBI-TaxID=180454 ;			
RN [1] -			
RP NUCLEOTIDE SEQUENCE.			
RC STRAIN=PEST;			
RG The Anopheles gambiae Sequence Committee;			
RT "Anopheles gambiae re-annotation.";			
RL Submitted (APR-2002) to the EMBL/GenBank/NCBI databases.			
RN [2]			
RP NUCLEOTIDE SEQUENCE.			
RC STRAIN=PEST;			
RG The Anopheles gambiae Sequence Committee;			
RL Submitted (APR-2004) to the EMBL/GenBank/NCBI databases.			
CC -!- CRUTION: The sequence shown here is derived from an			
CC EMBL/GenBank/NCBI whole genome shotgun (WGS) entry which is			
CC preliminary data.			
DR EAA04053.2; -; Genomic_DNA.			
FT NON_TER			
FT 208	208		
FT SEQUENCE	208 AA; 22236 MW; 0C842054742B1720 CRC64;		
Qy Query Match	Score 51; DB 2; Length 208;		
Best Local Similarity	60.0%;		
Matches	Pred. No. 19;		
8; Conservative	7; Mismatches 3; Indels 0;		
Qy Gaps	0;		
Db			
RESULT 9		Query Match	Score 49; DB 2; Length 110;
Q7U6KL_ SYNPK PRELIMINARY;	PRT; 294 AA.	Best Local Similarity	57.6%;
ID Q7U6KL_		Pred. No. 23;	
AC		Mismatches	2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)		Indels	0;
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)		Gaps	0;
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE ABC transporter component, possibly Mn transport.			
GN OrderedLocusName=SYNW1337;			
OS Synechococcus sp. (strain WH8102).			
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.			
NCBI-TaxID=84588			
RN [1]			
RP NUCLEOTIDE SEQUENCE.			
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943			
RA Palenik B.; Brahmshisa B.; Larimer F. W.; Land M. L.; Hauber L. ,			
RA Chain F.; Lamerdin J. E.; Regala W.; Allen E. E.; McCarren J. ,			
RA Paulsen I. T.; Dufresne A.; Partensky F.; Webb B. A.; Waterbury J. ,			
RA "The genome of a motile marine Synechococcus. ; ,			
RL Nature 424:1037-1042 (2003) ,			
DR EMBL: BX569692; CAE07852.1; -; Genomic_DNA.			
DR GO; GO:0016621; C:integral to membrane; IEA.			
DR GO: 00016620; C:membrane; IEA.			

RL Submitted (PEB-2005) to the EMBL/GenBank/DDJB databases.  
 DR EMBL: CP000050; AAY49380.1; -; Genomic\_DNA.  
 KW Heterochromatic protein.  
 SQ SEQUENCE 294 AA; 30273 MW; 6B9591AF17F215 CRC64;  
 Query Match 57.6%; Score 49; DB 2; Length 294;  
 Best Local Similarity 62.5%; Pred. No. 49;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
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 Db 1 MRYATLSSLSSAVCA 16  
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 ID Q9PB18\_XANCP PRELIMINARY;  
 AC 1  
 RC 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DB Hypothetical protein XCC1308;  
 CN Orderedhochusnames-XCC1308;  
 OS Xanthomonas campestris (pv. campestris).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OC NCBITAXID=340;  
 RN [1]  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=ATCC 33913 / NCPPB 528;  
 MEDLINE=2022445; PubMed=1204217; DOI=10.1038/417459a;  
 RA Silva A.C.R., Ferro J.A., Reinach F.C., Furlan L.R.,  
 RA Queiroz R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,  
 RA Almeida N.P.Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,  
 RA Camargo L.P., Camarote F.G., Cattaneo F., Cardozo J.,  
 RA Ciapina L.P., Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,  
 RA El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,  
 RA Ferro M.I.T., Formighieri E.F., Franco M.C., Gruber A.,  
 RA Katsuyama A.M., Kishi J.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rosai N.M.,  
 RA Martins C.F.M., Menidan J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spinola L.A.F., Tabita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White P.F.,  
 RA Setubal J.C., Kitajima J.P.,  
 RT "Comparison of the genomes of two *Xanthomonas* pathogens with differing  
 host specificities."  
 RT Nature 417:459-463 (2002).  
 RL EMBL: AE012230; AAM40606.1; -; Genomic DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 294 AA; 30273 MW; 6B9591AF17F215 CRC64;  
 Query Match 57.6%; Score 49; DB 2; Length 294;  
 Best Local Similarity 62.5%; Pred. No. 49;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MRYMILGLLAAVCS 16  
 Db 1 MRYATLSSLSSAVCA 16  
 RESULT 13  
 Q9V523 DROMB PRELIMINARY; PRT; 181 AA.  
 ID Q9V523\_DROMB PRELIMINARY;  
 AC 1  
 RC 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2001 (TREMBLrel. 16, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DB CG907-PA; isocform A (C9027-pb, isoform b) (LP09315p).  
 ORFNames=CG0027;  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC *Bukaryota*; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; *Drosophila*; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; *Drosophila*.  
 RN [1]  
 NUCLEOTIDE SEQUENCE.  
 MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt T., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champ M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Balliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolashakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Busam D.A., Butler J., Cadieu E., Center A., Chandra I.,  
 RA Burris K.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA Cherry J.M., Decher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,  
 RA de Pablo B., Delcher A., Doup L.B., Downes M., Dugan-Rocha S., Dunn P.,  
 RA Dobson K.J., Dobson K.J., Dugan-Rocha S., Dunkov B.C., Fleischmann W.,  
 RA Durbin R.J., Evangelista C.C., Ferrera S., Ferriera S., Fleischmann W.,  
 RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Murphy L., Muzny D.M., Nelson D.L., Nelson D.R.,  
 RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.R.,  
 RA Nelson D.R., Nelson P., Nixon K., Nusslein D.R., Parkel J.M., Reese M.G.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puriv V., Rees M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Schaefer P., Shen H.,  
 RA Shieh B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spadling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svartskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zheng L.,  
 RA Zhang X.H., Zheng P.N., Zhou W., Zhou X., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RT *Science* 287:2185-2195 (2000).  
 RN [2]  
 NUCLEOTIDE SEQUENCE.  
 MEDLINE=2424065; PubMed=12537568;  
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgeson A.,  
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
 RA Parkel S., Patel S., Pfeiffer B.D., Richards S., Soergren E.J.,  
 RA Svartskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
 RT "Finishing a whole-genome shotgun release 3 of the *Drosophila melanogaster* genome sequence,"  
 RT *Genome Biol.* 3:RESEARCH0079-RESEARCH0079 (2002).  
 RN [3]  
 NUCLEOTIDE SEQUENCE.  
 MEDLINE=22426070; PubMed=12537573;  
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Svartskas R.,  
 RA Patel S., Frise E., Hodgeson A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celinker S.E.,  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective,"  
 RT *Genome Biol.* 3:RESEARCH0084-1-RESEARCH0084-20 (2002).  
 RN [4]  
 NUCLEOTIDE SEQUENCE.  
 MEDLINE=22426669; PubMed=12537572;  
 RA Celinker S.E., Crobb M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Mibra S., Crobb M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Bayraktaroglu L., Whitfield E.J.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Berman B.P., Berman R.A.,  
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Shu S.Q.,





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:06:33 ; Search time 23 Seconds  
64.703 Million cell updates/sec

Title: US-10-031-008-7

Perfect score: 85 Sequence: 1 MRYMIGLALLAAVCSAA 18

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:  
4: /cgn2\_6/ptodata/1/iaa/HCTUS\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:  
6: /cgn2\_6/ptodata/1/iaa/backfilled1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	27	1 US-08-464-318-7	Sequence 7, Appli
2	85	100.0	27	1 US-08-464-314-7	Sequence 7, Appli
3	85	100.0	27	1 US-08-464-566-7	Sequence 7, Appli
4	85	100.0	27	1 US-09-070-029-2	Sequence 2, Appli
5	85	100.0	90	2 US-09-124-671-25	Sequence 25, Appli
6	85	100.0	109	2 US-09-124-671-23	Sequence 23, Appli
7	85	100.0	109	2 US-09-124-671-27	Sequence 27, Appli
8	81	95.3	109	2 US-09-124-671-29	Sequence 29, Appli
9	81	95.3	17	1 US-08-464-318-1	Sequence 1, Appli
10	81	95.3	17	1 US-08-471-41-1	Sequence 1, Appli
11	81	95.3	17	1 US-08-461-566-1	Sequence 1, Appli
12	80	94.1	31	2 US-09-653-18-74	Sequence 74, Appli
13	51	60.0	175	2 US-09-307-613-7	Sequence 7, Appli
14	51	60.0	175	2 US-10-200-559-7	Sequence 7, Appli
15	48	56.5	128	2 US-09-227-767-41350	Sequence 41350, A
16	48	56.5	128	2 US-09-270-767-5656	Sequence 5656, A
17	47	55.3	205	2 US-09-302-540-13846	Sequence 13846, A
18	47	55.3	305	2 US-09-489-039A-731	Sequence 731, Appli
19	47	55.3	370	2 US-09-767-32759	Sequence 32759, A
20	46	54.1	157	2 US-09-270-767-47976	Sequence 47976, A
21	46	52.9	367	2 US-09-250-991A-22612	Sequence 22612, A
22	45	51.8	485	2 US-09-328-32-8210	Sequence 8210, Appli
23	44	51.8	485	2 US-09-328-32-8210	Sequence 8210, Appli
24	43.5	51.2	195	2 US-09-252-991A-22429	Sequence 22429, A
25	43	50.6	208	2 US-09-248-796A-14596	Sequence 14596, A
26	43	50.6	319	2 US-10-028-051A-8	Sequence 8, Appli
27	42	49.4	168	2 US-09-376-113-5	Sequence 5, Appli

#### ALIGNMENTS

RESULT 1  
US-08-464-318-7  
Sequence 7, Application US/08464318  
; Patent No. 5733348  
; GENERAL INFORMATION:  
; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,  
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,  
; APPLICANT: YEWDELL, JONATHAN W  
; TITLE OF INVENTION: IMMUNOGENIC CHIMERICAS  
; COMPRISING NUCLEAR ACID SEQUENCES ENCODING  
; ENDOPLASMIC RETICULUM SIGNAL SEQUENCE  
; TITLES OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND  
; TITLES OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464-318  
; FILING DATE: 5-JUNE-1995  
; CLASSIFICATION: 514  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/032,902  
; FILING DATE: 17-MAR-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RICHARD W. BORK  
; REGISTRATION NUMBER: 3,6,459  
; REFERENCE/DOCKET NUMBER: 2026-4069US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-751-6800  
; TELEFAX: 212-751-6849  
; TELEX: 422792  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; US-08-464-318-7  
Query Match 100.0% ; Score 85; DB 1; Length 27;

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RESULT 2
US 08-471-341-7
; Sequence 7, Application US/08471341
; Patient No. 5846540
; GENERAL INFORMATION:
; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
; APPLICANT: YEVDELL, JONATHAN W.
; TITLE OF INVENTION: IMMUNOCOGENIC CHIMERICAS
; TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
; TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
; TITLE OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORGAN & FINNIGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; CITY: U. S. A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,341
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,902
; FILING DATE: 17 MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 7 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; US 08-471-341-7

Query Match 100.0%; Score 85; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gap 0;
GENERAL INFORMATION:
; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
; APPLICANT: YEVDELL, JONATHAN W.
; Sequence 7, Application US/08461566
; Patient No. 5856187
; GENERAL INFORMATION:
; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
; APPLICANT: YEVDELL, JONATHAN W.

RESULT 3
US 08-461-566-7
; Sequence 7, Application US/08461566
; Patient No. 5856187
; GENERAL INFORMATION:
; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
; APPLICANT: YEVDELL, JONATHAN W.

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; OTHER INFORMATION: and beta-gal epitope  
US-09-070-629-2

Query Match Score 85; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 5

US-09-124-671-25  
Sequence 25, Application US/09124671A

Patent No. 6160088

GENERAL INFORMATION:

APPLICANT: Rothman, James

APPLICANT: Maynew, Mark

APPLICANT: Hoe, Mee

TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488

CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 25

LENGTH: 90

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chimeric human pLB-KDEL

US-09-124-671-25

Query Match Score 85; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 6

US-09-124-671-23  
Sequence 23, Application US/09124671A

Patent No. 6160088

GENERAL INFORMATION:

APPLICANT: Rothman, James

APPLICANT: Maynew, Mark

APPLICANT: Hoe, Mee

TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488

CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 23

LENGTH: 109

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chimeric human COMP-KDEL

US-09-124-671-23

Query Match Score 85; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 7

US-09-124-671-27  
Sequence 27, Application US/09124671A

Patent No. 6160088

GENERAL INFORMATION:

APPLICANT: Rothman, James

APPLICANT: Maynew, Mark

APPLICANT: Hoe, Mee

TITLE OF INVENTION: chimeric human TSP3-KDEL

FILE REFERENCE: 31488

CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 27

LENGTH: 109

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chimeric human TSP3-KDEL

US-09-124-671-27

Query Match Score 85; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 8

US-09-124-671-29  
Sequence 29, Application US/09124671A

Patent No. 6160088

GENERAL INFORMATION:

APPLICANT: Rothman, James

APPLICANT: Maynew, Mark

APPLICANT: Hoe, Mee

TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488

CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 29

LENGTH: 109

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chimeric human TSP4-KDEL

US-09-124-671-29

Query Match Score 85; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRYMILGLLAAAVCSAA 18

RESULT 9

US-08-44-318-1  
Sequence 1, Application US/08464318

Patent No. 5733348

GENERAL INFORMATION:

APPLICANT: Restivo, Nicholas P.

APPLICANT: Rosenberger,

APPLICANT: Steven A., Bennink,

APPLICANT: Jack R., Braciuk, Igor,

APPLICANT: Jonathan W.

TITLE OF INVENTION: IMMUNOGENIC CHIMERIC

ACID SEQUENCES ENCODING

TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE  
 TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN & FINNEGAN  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 COUNTRY: U.S.A.  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,318  
 FILING DATE: 5-JUNE-1995  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/032,902  
 FILING DATE: 17-MAR-1993  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: RICHARD W. BORK  
 REGISTRATION NUMBER: 36,459  
 REFERENCE DOCKET NUMBER: 2026-4069US2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-758-4800  
 TELEX: 212-751-6849  
 TELEX: 421792  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 amino acid residues  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 US-08-464-318-1

Query Match 95.3%; Score 81; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
 US-08-471-341-1  
 Patent No. 5846540  
 GENERAL INFORMATION:  
 APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,  
 APPLICANT: STEVEN A. BENNINK, JACK R., BACTIK, IGOR,  
 APPLICANT: YEWDELL, JONATHAN W.  
 TITLE OF INVENTION: IMMUNOGENIC CHIMERICAS  
 TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING  
 TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE  
 TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND  
 TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN & FINNEGAN  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 COUNTRY: U.S.A.  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461,566  
 FILING DATE: 05-JUNE-1995  
 CLASSIFICATION: 424  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/032,902  
 FILING DATE: 17-MAR-1993  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: RICHARD W. BORK  
 REGISTRATION NUMBER: 36,459  
 REFERENCE DOCKET NUMBER: 2026-4069US3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-758-4800  
 TELEX: 212-751-6849  
 TELEX: 421792

INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acid residues  
; TYPE: amino acid  
; STRANDBEDNESS: unknown  
; TOPOLOGY: unknown  
; US-08-461-566-1

Query Match 95.3%; Score 81; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ 1 MRYMIGLALLAAVCSA 17  
Db 1 MRYMIGLALLAAVCSA 17

RESULT 14  
US-10-200-659-7  
; Sequence 7, Application US/10200659  
; Patent No. 6927279

GENERAL INFORMATION:  
; APPLICANT: Cupp, Eddie Wayne  
; TITLE OF INVENTION: Antithrombin Nucleotides and Proteins  
; TITLE OF INVENTION: From Horn Fly

FILE REFERENCE: 5721-10  
CURRENT APPLICATION NUMBER: US/10/200,659  
CURRENT FILING DATE: 2002-07-22  
PRIORITY APPLICATION NUMBER: US/09/376,113  
PRIORITY FILING DATE: 1999-08-17  
NUMBER OF SEQ ID NOS: 7  
SEQ ID NO 7  
SOFTWARE: FastSEQ for Windows Version 3.0  
; TYPE: PRT  
; ORGANISM: Haematobia Irritans  
US-10-200-659-7

Query Match 60.0%; Score 51; DB 2; Length 17;  
Best Local Similarity 53.3%; Pred. No. 0.67e-07;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
SEQ 3 YMIGLALLAAVCSA 17  
Db 4 FVVGIGLALLAAVCSA 18

RESULT 15  
US-09-210-767-41350  
; Sequence 41350, Application US/09270767  
; Patent No. 6703491

GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 6217  
SEQ ID NO 41350  
SOFTWARE: PatentIn Ver. 2.0  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: *Drosophila melanogaster*  
US-09-210-767-41350

Query Match 94.1%; Score 80; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ 2 RYMIGLALLAAVCSA 18  
Db 15 RYMIGLALLAAVCSA 31

RESULT 13  
US-09-376-113-7  
; Sequence 7, Application US/09376113  
; Patent No. 6451992

GENERAL INFORMATION:  
; APPLICANT: Cupp, Eddie Wayne  
; TITLE OF INVENTION: Antithrombin Nucleotides and Proteins  
; TITLE OF INVENTION: From Horn Fly  
FILE REFERENCE: 5721-10  
CURRENT APPLICATION NUMBER: US/09/376,113  
CURRENT FILING DATE: 1999-08-17  
NUMBER OF SEQ ID NOS: 7  
SEQ ID NO 7  
SOFTWARE: FastSEQ for Windows Version 3.0  
; LENGTH: 175  
; TYPE: PRT

Query Match 56.5%; Score 48; DB 2; Length 128;  
Best Local Similarity 51.3%; Pred. No. 1.5e-07;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
SEQ 1 MRYMIGLALLAAVC 15  
Db 72 IRMVIGTVALLVC 86

Search completed: January 11, 2006, 00:10:38  
Job time : 23 secs

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: January 11, 2006, 00:09:44 ; Search time 61 Seconds (without alignments)

123,294 Million cell updates/sec

Title: US-10-031-008-7

Perfect score: 85

Sequence: 1 MRYMIGLLAAVCSAA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA Main:\*

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2: /cgpn2\_6/podata/1/pubpaas/us08\_pubcomb.pep:\*

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4: /cgpn2\_6/podata/1/pubpaas/us10\_pubcomb.pep:\*

5: /cgpn2\_6/podata/1/pubpaas/us10b\_pubcomb.pep:\*

6: /cgpn2\_6/podata/1/pubpaas/us11\_pubcomb.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	18	3 US-09-894-594-65	Sequence 65, Appl
2	85	100.0	18	3 US-09-894-594-70	Sequence 70, Appl
3	85	100.0	18	4 US-10-080-597-13	Sequence 13, Appl
4	85	100.0	27	5 US-10-848-520-2	Sequence 2, Appl
5	85	100.0	90	5 US-10-915-514-25	Sequence 25, Appl
6	85	100.0	90	5 US-10-873-530-25	Sequence 25, Appl
7	85	100.0	90	5 US-10-873-594-25	Sequence 23, Appl
8	85	100.0	109	4 US-10-815-514-23	Sequence 27, Appl
9	85	100.0	109	4 US-10-815-514-27	Sequence 29, Appl
10	85	100.0	109	4 US-10-815-514-29	Sequence 23, Appl
11	85	100.0	109	5 US-10-877-530-23	Sequence 27, Appl
12	85	100.0	109	5 US-10-877-530-27	Sequence 29, Appl
13	85	100.0	109	5 US-10-877-530-29	Sequence 23, Appl
14	85	100.0	109	5 US-10-873-594-23	Sequence 27, Appl
15	85	100.0	109	5 US-10-873-594-27	Sequence 29, Appl
16	85	100.0	109	5 US-10-873-594-29	Sequence 2, Appl
17	82	96.5	26	4 US-10-331-163-2	Sequence 74, Appl
18	80	94.1	31	4 US-10-715-869-74	Sequence 74, Appl
19	80	94.1	31	4 US-10-366-933-74	Sequence 74, Appl
20	80	94.1	31	5 US-10-926-993-74	Sequence 74, Appl
21	51	60.0	175	4 US-10-20-659-7	Sequence 7, Appl
22	48	56.5	179	6 US-11-097-143-19317	Sequence 28580, A
23	48	56.5	181	6 US-11-097-143-24680	Sequence 8319, Ap
24	46	54.1	140	4 US-10-156-761-8319	Sequence 21653, Ap
25	46	54.1	148	4 US-10-424-599-216653	Sequence 74, Appl
26	46	54.1	5175	4 US-10-120-801-74	Sequence 6859, Ap
27	46	54.1	5175	4 US-10-369-493-6859	Sequence 240570, A

## ALIGNMENTS

RESULT: 1  
US-09-894-594-65  
; Sequence 65, Application US/09894594  
; Publication No. US20030017497A1  
; GENERAL INFORMATION:  
; APPLICANT: Kieber-Emmons, Thomas  
; APPLICANT: Werner, David B.  
; APPLICANT: Monzavi, Karbassi, Behjatolah  
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encoded by RNA  
; FILE REFERENCE: UPN-3984  
; CURRENT APPLICATION NUMBER: US/09-894, 594  
; CURRENT FILING DATE: 2001-06-28  
; PRIORITY APPLICATION NUMBER: 09/601, 558  
; PRIORITY FILING DATE: 2000-11-07  
; PRIORITY APPLICATION NUMBER: PCT/US99/024405  
; PRIORITY FILING DATE: 1999-02-04  
; PRIORITY APPLICATION NUMBER: 60/073, 690  
; PRIORITY FILING DATE: 1998-02-04  
; PRIORITY APPLICATION NUMBER: 60/214, 517  
; PRIORITY FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 65  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Novel Sequence  
US-09-894-594-65

Query Match 100.0% ; Score 85; DB 3; Length 18;  
Best local similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 1 MRYMILGLLAAVCSAA 18  
Db 1 MRYMILGLLAAVCSAA 18

RESULT: 2  
US-09-894-594-70  
; Sequence 70, Application US/09894594  
; Publication No. US20030017497A1  
; GENERAL INFORMATION:  
; APPLICANT: Kieber-Emmons, Thomas  
; APPLICANT: Werner, David B.  
; APPLICANT: Monzavi, Karbassi, Behjatolah  
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encoded by RNA



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; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO: 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-031-008-7.rapbm

Query Match 100.0%; Score 85; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: DOMAIN
Qy 1 MRYMILGILALAAVCSAA 18
Db 1 MRYMILGILALAAVCSAA 18

RESULT 7
US-10-031-008-7.rapbm

Query Match 100.0%; Score 85; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: DOMAIN
Qy 1 MRYMILGILALAAVCSAA 18
Db 1 MRYMILGILALAAVCSAA 18

RESULT 8
US-10-031-514-23
; Sequence 23, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-1-I 065360_0152
; CURRENT APPLICATION NUMBER: US/10/873,594
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/800,358
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/696,070
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/124,671
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO: 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric KDEL receptor inhibitor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) .. (20)
; OTHER INFORMATION: Cleavable leader/signal peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (6) .. (9)
; OTHER INFORMATION: The sub-sequence GDDC
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (10) .. (16)
; OTHER INFORMATION: human PLB pentamerization domain
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (13) .. (13)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (18) .. (18)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (21) .. (21)
; OTHER INFORMATION: Critical for pentamer formation

Query Match 100.0%; Score 85; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: DOMAIN
Qy 1 MRYMILGILALAAVCSAA 18
Db 1 MRYMILGILALAAVCSAA 18

RESULT 9
US-10-031-514-27
; Sequence 27, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO: 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human COMP-KDEL

Query Match 100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: DOMAIN
Qy 1 MRYMILGILALAAVCSAA 18
Db 1 MRYMILGILALAAVCSAA 18

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; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: chimeric human TSP3-KDEL
; US-10-815-314-27

Query Match 100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-815-314-27
; Sequence 29, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 29
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: chimeric human TSP3-KDEL
; US-10-815-314-29

Query Match 100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 13
US-10-817-930-29
; Sequence 29, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 29
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: chimeric human TSP3-KDEL
; US-10-817-930-29

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 14
US-10-817-930-27
; Sequence 27, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: chimeric human TSP3-KDEL
; US-10-817-930-27

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 15
US-10-817-930-29
; Sequence 29, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: chimeric human TSP4-KDEL
; US-10-817-930-29

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MRYMILGLALAAVCSAA 18  
 Db 1 MRYMILGLALAAVCSAA 18

RESULT 14  
 US-10-873-594-23  
 Sequence 23, Application US/10873594  
 GENERAL INFORMATION: Publication No. US2005009567A1  
 APPLICANT: Rothman, James  
 APPLICANT: Maynew, Mark  
 APPLICANT: Hoe, Mee  
 TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
 FILE REFERENCE: A31488-1-I 065360-0152  
 CURRENT APPLICATION NUMBER: US/10-873-594  
 CURRENT FILING DATE: 2004-06-21  
 PRIOR APPLICATION NUMBER: US/09/800,358  
 PRIOR FILING DATE: 2001-03-05  
 PRIOR APPLICATION NUMBER: 09/696,070  
 PRIOR FILING DATE: 2000-10-25  
 NUMBER OF SEQ ID NOS: 42  
 SEQ ID NO: 23  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Chimeric KDEL receptor inhibitor  
 NAME/KEY: SIGNAL  
 LOCATION: (1) .. (20)  
 OTHER INFORMATION: Cleavable leader/signal peptide  
 FEATURE:  
 OTHER INFORMATION: Chimeric KDEL receptor inhibitor  
 NAME/KEY: SIGNAL  
 LOCATION: (1) .. (20)  
 OTHER INFORMATION: Cleavable leader/signal peptide  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (1) .. (3)  
 OTHER INFORMATION: Linker  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (1) .. (20)  
 OTHER INFORMATION: Cleavable leader/signal peptide  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (1) .. (9)  
 OTHER INFORMATION: The sub-sequence GDCC  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (10) .. (55)  
 OTHER INFORMATION: human TSP3 trimerization domain  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (6) .. (9)  
 OTHER INFORMATION: The sub-sequence GDCC  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (56) .. (79)  
 OTHER INFORMATION: Camel IgG linker domain  
 US-10-873-594-27

Query Match 100.0%; Score 85; DB 5; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 5e-05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLALAAVCSAA 18  
 Db 1 MRYMILGLALAAVCSAA 18

RESULT 15  
 US-10-873-594-27  
 Sequence 27, Application US/10873594  
 Publication No. US2005009566A1  
 GENERAL INFORMATION:  
 APPLICANT: Rothman, James  
 APPLICANT: Maynew, Mark  
 APPLICANT: Hoe, Mee  
 TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
 FILE REFERENCE: A31488-1-I 065360-0152

Search completed: January 11, 2006, 00:19:38  
 Job time : 62 secs

Query Match 100.0%; Score 85; DB 5; Length 109;  
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Qy 1 MRYMILGLALAAVCSAA 18  
 Db 1 MRYMILGLALAAVCSAA 18

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1	43	50.6	319	7	US-11-184-005-8	Sequence 8, Appli	Sequence 31, Appli	Sequence 31, Appli	Sequence 31, Appli
2	41	48.2	152	7	US-11/000	Sequence 31, Appli	Sequence 31, Appli	Sequence 31, Appli	Sequence 31, Appli
3	40	47.1	325	7	US-11-184-005-2	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli
4	40	47.1	824	6	US-10-821-234-1008	Sequence 1008, Appli	Sequence 1008, Appli	Sequence 1008, Appli	Sequence 1008, Appli
5	40	47.1	819	7	US-11-000-46-819	Sequence 819, Appli	Sequence 820, Appli	Sequence 820, Appli	Sequence 820, Appli
6	39	45.9	74	7	US-11-000-46-820	Sequence 820, Appli	Sequence 820, Appli	Sequence 820, Appli	Sequence 820, Appli
7	39	45.9	331	7	US-11-143-980-57	Sequence 57, Appli	Sequence 57, Appli	Sequence 57, Appli	Sequence 57, Appli
8	39	45.9	502	7	US-11-112-240-158	Sequence 158, Appli	Sequence 158, Appli	Sequence 158, Appli	Sequence 158, Appli
9	39	45.9	1061	7	US-11-000-467-347	Sequence 347, Appli	Sequence 347, Appli	Sequence 347, Appli	Sequence 347, Appli
10	39	45.9	1091	7	US-11-000-463-348	Sequence 348, Appli	Sequence 348, Appli	Sequence 348, Appli	Sequence 348, Appli
11	39	45.9	143	7	US-11-186-284-117	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli
12	38	44.7	163	7	US-11-102-240-160	Sequence 18, Appli	Sequence 18, Appli	Sequence 18, Appli	Sequence 18, Appli
13	37	44.1	618	7	US-11-078-735-18	Sequence 161, Appli	Sequence 161, Appli	Sequence 161, Appli	Sequence 161, Appli
14	37	43.5	243	6	US-10-821-234-11661	Sequence 118, Appli	Sequence 118, Appli	Sequence 118, Appli	Sequence 118, Appli
15	37	43.5	243	6	US-10-830-5562-1118	Sequence 1286, Appli	Sequence 1286, Appli	Sequence 1286, Appli	Sequence 1286, Appli
16	37	43.5	861	6	US-10-467-657-1286	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli
17	36	42.4	143	7	US-11-186-284-117	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli
18	36	42.4	350	6	US-10-878-528-132	Sequence 338, Appli	Sequence 338, Appli	Sequence 338, Appli	Sequence 338, Appli
19	36	42.4	390	6	US-10-131-822A-338	Sequence 320, Appli	Sequence 320, Appli	Sequence 320, Appli	Sequence 320, Appli
20	36	42.4	548	6	US-10-055-877-320	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli	Sequence 117, Appli
21	36	42.4	675	6	US-10-055-877-317	Sequence 317, Appli	Sequence 317, Appli	Sequence 317, Appli	Sequence 317, Appli
22	36	42.4	146	7	US-11-000-463-881	Sequence 881, Appli	Sequence 881, Appli	Sequence 881, Appli	Sequence 881, Appli
23	35	41.2	181	7	US-11-097-622-110	Sequence 409, Appli	Sequence 409, Appli	Sequence 409, Appli	Sequence 409, Appli
24	35	41.2	158	7	US-11-000-463-409	Sequence 105, Appli	Sequence 105, Appli	Sequence 105, Appli	Sequence 105, Appli

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; CURRENT FILING DATE: 2004-12-23
; PRIORITY APPLICATION NUMBER: US 09/249,542
; PRIORITY FILING DATE: 1999-02-12
; PRIORITY APPLICATION NUMBER: US 60/074,640
; PRIORITY FILING DATE: 1998-02-13
; PRIORITY APPLICATION NUMBER: US 08/853,703
; PRIORITY FILING DATE: 1997-05-09
; PRIORITY APPLICATION NUMBER: US 08/729,452
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO: 31
; LENGTH: 152
; TYPE: PRT
; OTHER INFORMATION: HIV antisense HAP protein translated from AUG start; requires -1
; FEATURE: human immunodeficiency virus of Clade A
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HIV antisense HAP protein translated from AUG start; requires -1
; US 11/020,772-31
; SEQ ID NO: 31
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-184-005-4

; Query Match 48.2%; Score 41; DB 7; Length 152;
; Best Local Similarity 46.7%; Prod. No. 3.5;
; Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
; Qy 4 MLLGLAAVCSAA 18
; Db 102 MLVGIWSLALVCNSA 116

RESULT 3
US-11-184-005-2
; Sequence 2, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; FILE REFERENCE: NIH133_1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIORITY APPLICATION NUMBER: US 10/028051
; PRIORITY FILING DATE: 2001-12-19
; PRIORITY APPLICATION NUMBER: US 08/822333
; PRIORITY FILING DATE: 1997-03-20
; PRIORITY APPLICATION NUMBER: US 08/729,452
; PRIORITY FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Bos taurus
; US-11-184-005-2

; Query Match 47.1%; Score 40; DB 7; Length 325;
; Best Local Similarity 88.9%; Prod. No. 11;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; Qy 7 GLLLAAVCSA 15
; Db 15 GLLLAAALC 23

RESULT 4
US-11-184-005-4
; Sequence 4, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; FILE REFERENCE: NIH133_1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIORITY APPLICATION NUMBER: US 10/028051
; PRIORITY FILING DATE: 2001-12-19
; PRIORITY APPLICATION NUMBER: US 08/822333
; PRIORITY FILING DATE: 1997-03-20
; PRIORITY APPLICATION NUMBER: US 08/729,452
; PRIORITY FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-184-005-4

; Query Match 47.1%; Score 40; DB 7; Length 325;
; Best Local Similarity 88.9%; Prod. No. 11;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; Qy 7 GLLLAAVCSA 15
; Db 15 GLLLAAALC 23

RESULT 5
US-10-821-234-1008
; Sequence 1008, Application US/10821234
; Publication No. US2005025514A1
; GENERAL INFORMATION:
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIORITY APPLICATION NUMBER: US 60/462,047
; PRIORITY FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO: 1006
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1008

; Query Match 47.1%; Score 40; DB 6; Length 824;
; Best Local Similarity 88.9%; Prod. No. 30;
; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; Qy 6 GLLLAAVCSA 17
; Db 55 GLLLAAVAAA 66

RESULT 6
US-11-000-463-819
; Sequence 819, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Lai, Ming

; Query Match 47.1%; Score 40; DB 6; Length 824;
; Best Local Similarity 88.9%; Prod. No. 30;
; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; Qy 6 GLLLAAVCSA 17
; Db 55 GLLLAAVAAA 66

```

APPLICANT: Drmanac, Radoje T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785CIPACN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 PRIOR FILING DATE: 2000-09-15  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 819  
 LENGTH: 74  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-819

Query Match 45.9%; Score 39; DB 7; Length 74;  
 Best Local Similarity 50.0%; Pred. No. 3.4%;  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MILGLLAAVC 15  
 Db 1 MVVGIVAAALC 12

RESULT 7  
 US-11-000-463-820  
 Sequence 820, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhwei  
 APPLICANT: Wenzman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Drmanac, Radoje T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785CIPACN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 820

; LENGTH: 74  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-000-463-820  
 Query Match 45.9%; Score 39; DB 7; Length 74;  
 Best Local Similarity 50.0%; Pred. No. 3.4%;  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 Qy 4 MILGLLAAVC 15  
 Db 1 MVVGIVAAALC 12

RESULT 8  
 US-11-143-980-57  
 Sequence 57, Application US/1143980  
 Publication No. US20050272133A1  
 GENERAL INFORMATION:  
 ; APPLICANT: He, Min  
 ; APPLICANT: Hucul, John  
 ; APPLICANT: Hultli, Bradley A.  
 ; APPLICANT: Wagenaar, Melissa M.  
 ; APPLICANT: Graziani, Edmund  
 ; APPLICANT: Summers, Mia  
 ; APPLICANT: Kuliowski, Kerry  
 ; APPLICANT: Pong, Kevin  
 ; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex  
 ; FILE REFERENCE: AM-101426US  
 ; CURRENT APPLICATION NUMBER: US/11/143,980  
 ; CURRENT FILING DATE: 2005-06-03  
 ; PRIOR APPLICATION NUMBER: US 60/664,483  
 ; PRIOR FILING DATE: 2005-03-23  
 ; PRIOR APPLICATION NUMBER: US 60/576,895  
 ; PRIOR FILING DATE: 2004-06-03  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO: 57  
 ; LENGTH: 331  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces sp.  
 US-11-143-980-57

Query Match 45.9%; Score 39; DB 7; Length 331;  
 Best Local Similarity 56.2%; Pred. No. 16;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 YMIGLGLAAVC 18  
 Db 192 YLGNGLGLAAVC 207

RESULT 9  
 US-11-102-240-158  
 Sequence 158, Application US/11102240  
 Publication No. US2005026647A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Goowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Wood, William J.  
 ; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES  
 ; FILE REFERENCE: P3230R1C106C  
 ; CURRENT APPLICATION NUMBER: US/11/102,240  
 ; CURRENT FILING DATE: 2005-04-08  
 ; PRIOR APPLICATION NUMBER: 10/063662  
 ; PRIOR FILING DATE: 2002-05-07  
 ; PRIOR APPLICATION NUMBER: 10/006867  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: 60/170262  
 PRIORITY FILING DATE: 199-12-09  
 NUMBER OF SEQ ID NOS: 170  
 SEQ ID NO: 158  
 LENGTH: 502  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-11-102-240-158

Query Match 45.9%; Score 39; DB 7; Length 502;  
 Best Local Similarity 60.0%; Pred. No. 26;  
 Matches 3; Mismatches 0; Gaps 0;  
 Indels 3;

Qy 4 MIGLLAAAVCSAA 18  
 Db 1 MSLVLLSIALCRSA 15

RESULT 10  
 Sequence 347, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Drimnac, Radoe T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785C1P4CN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 PRIOR FILING DATE: 2000-09-15  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 348  
 LENGTH: 1091  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-348

Query Match 45.9%; Score 39; DB 7; Length 1091;  
 Best Local Similarity 50.0%; Pred. No. 58;  
 Matches 6; Mismatches 5; Indels 0; Gaps 0;

Qy 4 MILGLIAAVC 15  
 Db 1018 MVVGIVAAAALC 1029

RESULT 12  
 Sequence 160, Application US/1102240  
 Publication No. US2005026647A1  
 GENERAL INFORMATION:  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurine, Austin L.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS:  
 FILE REFERENCE: P3230RLC106C  
 CURRENT APPLICATION NUMBER: US/11/102,240  
 CURRENT FILING DATE: 2005-04-08  
 PRIOR APPLICATION NUMBER: 10/063,662  
 PRIOR FILING DATE: 2002-05-07  
 PRIOR APPLICATION NUMBER: 10/006867  
 PRIOR FILING DATE: 2001-12-06  
 PRIOR APPLICATION NUMBER: PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: 60/170262  
 NUMBER OF SEQ ID NOS: 170  
 SEQ ID NO: 160

Query Match 45.9%; Score 39; DB 7; Length 1061;  
 Best Local Similarity 50.0%; Pred. No. 56;  
 Matches 6; Mismatches 5; Indels 0; Gaps 0;

Qy 4 MIGLLAAAVC 15  
 Db 988 MVVGIVAAAALC 999

RESULT 11  
 Sequence 348, Application US/11000463  
 US-11-000-463-348

LENGTH: 163  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-11-024-160

Query Match 44.7%; Score 38; DB 7; Length 163;  
 Best Local Similarity 38.9%; Pred. No. 11;  
 Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRYMLGLALAACSA 18  
 ::|:| :| :|:  
 Db 12 VRYLLSILGLAFLESEA 29

RESULT 13  
 US-11-018-735-18  
 Sequence 18. Application US/11078735  
 Publication No. US20050261477A1

GENERAL INFORMATION:  
 APPLICANT: CHAMPION, BRIAN ROBERT  
 APPLICANT: LENNARD, ANDREW CHRISTOPHER  
 APPLICANT: MCKENZIE, GRAHAME JAMES  
 APPLICANT: TUGAL, TAMARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS  
 TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS  
 FILE REFERENCE: 674525-2019

CURRENT APPLICATION NUMBER: US/11/078,735  
 CURRENT FILING DATE: 2005-03-10  
 PRIOR APPLICATION NUMBER: PCT/GB03/03908  
 PRIOR FILING DATE: 2003-09-09  
 PRIOR APPLICATION NUMBER: PCT/GB03/03285  
 PRIOR FILING DATE: 2003-08-01  
 PRIOR APPLICATION NUMBER: PCT/GB03/01525  
 PRIOR FILING DATE: 2003-04-04  
 PRIOR APPLICATION NUMBER: GB 0300234.2  
 PRIOR FILING DATE: 2003-01-07  
 PRIOR APPLICATION NUMBER: PCT/GB02/05137  
 PRIOR FILING DATE: 2002-11-13  
 PRIOR APPLICATION NUMBER: PCT/GB02/05133  
 PRIOR FILING DATE: 2002-11-13  
 PRIOR APPLICATION NUMBER: GB 0220912.0  
 PRIOR FILING DATE: 2002-09-10  
 PRIOR APPLICATION NUMBER: GB 0220913.8  
 PRIOR FILING DATE: 2002-09-10  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: PatentIn Ver. 3.3  
 SEQ ID NO: 18  
 LENGTH: 618  
 TYPE: PRT  
 ORGANISM: Homo Sapiens  
 US-11-078-735-18

Query Match 44.1%; Score 37.5; DB 7; Length 618;  
 Best Local Similarity 50.0%; Pred. No. 56;  
 Matches 10; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

Qy 2 RYMI--LGILALAAVCSA 18  
 ::|:| :| :|:  
 Db 4 90 RYLLPAGLVAAGVAGAA 509

RESULT 14  
 US-10-821-234-1661  
 Sequence 1661, Application US/10821234  
 Publication No. US20050255114A1

GENERAL INFORMATION:  
 APPLICANT: Labat, Ivan  
 APPLICANT: Stache-Crain, Birgit  
 APPLICANT: Andamani, Susan  
 APPLICANT: Tang, Y. Tom  
 TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 FILE REFERENCE: 821A  
 CURRENT APPLICATION NUMBER: US/10/821,234

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